

CB



PCT09

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/857,308

DATE: 03/13/2002 05  
 TIME: 13:52:58

Input Set : A:\0020-4872P.ST25.txt  
 Output Set: N:\CRF3\03132002\I857308.raw

3 <110> APPLICANT: ITOH, Kyogo et al.  
 5 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN PROTEIN ART-1 AND TUMOR ANTIGEN PEPTIDES  
 THEREOF

7 <130> FILE REFERENCE: 0020-4872P  
 9 <140> CURRENT APPLICATION NUMBER: US 09/857,308  
 C--> 10 <141> CURRENT FILING DATE: 2001-09-18  
 12 <150> PRIOR APPLICATION NUMBER: Japan: 98-341253  
 13 <151> PRIOR FILING DATE: 1998-12-01  
 15 <160> NUMBER OF SEQ ID NOS: 21  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 414  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Homo sapiens  
 22 <400> SEQUENCE: 1  
 23 Met Asn Leu Gln Arg Tyr Trp Gly Glu Ile Pro Ile Ser Ser Ser Gln  
 24 5 10 15  
 25 Thr Asn Arg Ser Ser Phe Asp Leu Leu Pro Arg Glu Phe Arg Leu Val  
 26 20 25 30  
 27 Glu Val His Asp Pro Pro Leu His Gln Pro Ser Ala Asn Lys Pro Lys  
 28 35 40 45  
 29 Pro Pro Thr Met Leu Asp Ile Pro Ser Glu Pro Cys Ser Leu Thr Ile  
 30 50 55 60  
 31 His Thr Ile Gln Leu Ile Gln His Asn Arg Arg Leu Arg Asn Leu Ile  
 32 65 70 75 80  
 33 Ala Thr Ala Gln Ala Gln Asn Gln Gln Thr Glu Gly Val Lys Thr  
 34 85 90 95  
 35 Glu Glu Ser Glu Pro Leu Pro Ser Cys Pro Gly Ser Pro Pro Leu Pro  
 36 100 105 110  
 37 Asp Asp Leu Leu Pro Leu Asp Cys Lys Asn Pro Asn Ala Pro Phe Gln  
 38 115 120 125  
 39 Ile Arg His Ser Asp Pro Glu Ser Asp Phe Tyr Arg Gly Lys Gly Glu  
 40 130 135 140  
 41 Pro Val Thr Glu Leu Ser Trp His Ser Cys Arg Gln Leu Leu Tyr Gln  
 42 145 150 155 160  
 43 Ala Val Ala Thr Ile Leu Ala His Ala Gly Phe Asp Cys Ala Asn Glu  
 44 165 170 175  
 45 Ser Val Leu Glu Thr Leu Thr Asp Val Ala His Glu Tyr Cys Leu Lys  
 46 180 185 190  
 47 Phe Thr Lys Leu Leu Arg Phe Ala Val Asp Arg Glu Ala Arg Leu Gly  
 48 195 200 205  
 49 Gln Thr Pro Phe Pro Asp Val Met Glu Gln Val Phe His Glu Val Gly  
 50 210 215 220  
 51 Ile Gly Ser Val Leu Ser Leu Gln Lys Phe Trp Gln His Arg Ile Lys  
 52 225 230 235 240

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53 Asp Tyr His Ser Tyr Met Leu Gln Ile Ser Lys Gln Leu Ser Glu Glu  
54 245 250 255  
55 Tyr Glu Arg Ile Val Asn Pro Glu Lys Ala Thr Glu Asp Ala Lys Pro  
56 260 265 270  
57 Val Lys Ile Lys Glu Glu Pro Val Ser Asp Ile Thr Phe Pro Val Ser  
58 275 280 285  
59 Glu Glu Leu Glu Ala Asp Leu Ala Ser Gly Asp Gln Ser Leu Pro Met  
60 290 295 300  
61 Gly Val Leu Gly Ala Gln Ser Glu Arg Phe Pro Ser Asn Leu Glu Val  
62 305 310 315 320  
63 Glu Ala Ser Pro Gln Ala Ser Ser Ala Glu Val Asn Ala Ser Pro Leu  
64 325 330 335  
65 Trp Asn Leu Ala His Val Lys Met Glu Pro Gln Glu Ser Glu Glu Gly  
66 340 345 350  
67 Asn Val Ser Gly His Gly Val Leu Gly Ser Asp Val Phe Glu Glu Pro  
68 355 360 365  
69 Met Ser Gly Met Ser Glu Ala Gly Ile Pro Gln Ser Pro Asp Asp Ser  
70 370 375 380  
71 Asp Ser Ser Tyr Gly Ser His Ser Thr Asp Ser Leu Met Gly Ser Ser  
72 385 390 395 400  
73 Pro Val Phe Asn Gln Arg Cys Lys Lys Arg Met Arg Lys Ile  
74 405 410  
76 <210> SEQ ID NO: 2  
77 <211> LENGTH: 1711  
78 <212> TYPE: DNA  
79 <213> ORGANISM: Homo sapiens  
81 <400> SEQUENCE: 2  
82 acgcgatcct tgcctcaggc ctctcgaggt ccagacagcc gcccagcccg ctctgcgacg 60  
83 cagcagtcaa tagtgtggta cctccttgc tcggttcagg tccagacactc cccgtcttcc 120  
84 ggctgcctcg aacgtcaggc gacctcagga ccctgtgatt ggccgcctgcg cggcggacc 180  
85 gtgaccgagg aaaccctgg agggacttgg gcattcccttg ggctccgtgc ctgttcttcg 240  
86 tgctcccttc gggcaaggat ctcacattat cagtcattga ccgacacaga atgcctggca 300  
87 tttgataaat gtttgtgaa cttgaagaga catatggaca atg aat ctg caa aga 355  
88 Met Asn Leu Gln Arg 5  
89  
90 tac tgg gga gag ata cca ata tca tca agc cag acc aac aga agt tcc 403  
91 Tyr Trp Gly Glu Ile Pro Ile Ser Ser Gln Thr Asn Arg Ser Ser  
92 10 15 20  
93 ttc gat ttg ctc cca cgg gag ttc cgt ctg gtg gaa gtc cat gac cca 451  
94 Phe Asp Leu Leu Pro Arg Glu Phe Arg Leu Val Glu Val His Asp Pro  
95 25 30 35  
96 ccc ctg cac caa ccc tca gcc aac aag ccg aag ccc ccc act atg ctg 499  
97 Pro Leu His Gln Pro Ser Ala Asn Lys Pro Lys Pro Pro Thr Met Leu  
98 40 45 50  
99 gac atc ccc tca gag cca tgt agt ctc acc atc cat acg att cag ttg 547  
100 Asp Ile Pro Ser Glu Pro Cys Ser Leu Thr Ile His Thr Ile Gln Leu  
101 55 60 65  
102 att cag cac aac cga cgt ctt cgc aac ctt att gcc aca gct cag gcc 595  
103 Ile Gln His Asn Arg Arg Leu Arg Asn Leu Ile Ala Thr Ala Gln Ala

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104	70	75	80	85	
105	cag aat cag cag aca gaa ggt gta aaa act gaa gag agt gaa cct				643
106	Gln Asn Gln Gln Thr Glu Gly Val Lys Thr Glu Glu Ser Glu Pro				
107	90	95		100	
108	ctt ccc tcg tgc cct ggg tca cct ctc cct gat gac ctc ctg cct				691
109	Leu Pro Ser Cys Pro Gly Ser Pro Pro Leu Pro Asp Asp Leu Leu Pro				
110	105	110		115	
111	tta gat tgt aag aat ccc aat gca cca ttc cag atc cgg cac agt gac				739
112	Leu Asp Cys Lys Asn Pro Asn Ala Pro Phe Gln Ile Arg His Ser Asp				
113	120	125		130	
114	cca gag agt gac ttt tat cgt ggg aaa ggg gaa cct gtg act gaa ctc				787
115	Pro Glu Ser Asp Phe Tyr Arg Gly Lys Gly Glu Pro Val Thr Glu Leu				
116	135	140		145	
117	agc tgg cac tcc tgt cgg cag ctc ctc tac cag gca gtg gcc aca atc				835
118	Ser Trp His Ser Cys Arg Gln Leu Leu Tyr Gln Ala Val Ala Thr Ile				
119	150	155		160	165
120	ctg gcc cac gcg ggc ttt gac tgt gct aat gag agt gtc ctg gag acc				883
121	Leu Ala His Ala Gly Phe Asp Cys Ala Asn Glu Ser Val Leu Glu Thr				
122	170	175		180	
123	cta act gat gtg gca cat gag tat tgc ctt aag ttt acc aag ttg ctg				931
124	Leu Thr Asp Val Ala His Glu Tyr Cys Leu Lys Phe Thr Lys Leu Leu				
125	185	190		195	
126	cgt ttt gct gtg gac cgg gag gcc cgg ctg gga cag act cct ttt cct				979
127	Arg Phe Ala Val Asp Arg Glu Ala Arg Leu Gly Gln Thr Pro Phe Pro				
128	200	205		210	
129	gat gtg atg gag cag gta ttc cat gaa gtg ggt att ggc agt gtg ctc				1027
130	Asp Val Met Glu Gln Val Phe His Glu Val Gly Ile Gly Ser Val Leu				
131	215	220		225	
132	tcc ctc cag aag ttc tgg cag cac cgc atc aag gac tat cac agt tac				1075
133	Ser Leu Gln Lys Phe Trp Gln His Arg Ile Lys Asp Tyr His Ser Tyr				
134	230	235		240	245
135	atg cta cag att agt aag caa ctc tct gaa gaa tat gaa agg att gtc				1123
136	Met Leu Gln Ile Ser Lys Gln Leu Ser Glu Glu Tyr Glu Arg Ile Val				
137	250	255		260	
138	aat cct gag aag gcc aca gag gac gct aaa cct gtg aag atc aag gag				1171
139	Asn Pro Glu Lys Ala Thr Glu Asp Ala Lys Pro Val Lys Ile Lys Glu				
140	265	270		275	
141	gaa cct gtg agc gac atc act ttt cct gtc agt gag gag ctg gag gct				1219
142	Glu Pro Val Ser Asp Ile Thr Phe Pro Val Ser Glu Glu Leu Glu Ala				
143	280	285		290	
144	gac ctt gct tct gga gac cag tca ctg cct atg gga gtg ctt ggg gct				1267
145	Asp Leu Ala Ser Gly Asp Gln Ser Leu Pro Met Gly Val Leu Gly Ala				
146	295	300		305	
147	cag agc gaa cgc ttc cca tct aac ctg gag gtt gaa gct tca cca cag				1315
148	Gln Ser Glu Arg Phe Pro Ser Asn Leu Glu Val Glu Ala Ser Pro Gln				
149	310	315		320	325
150	gct tca agt gca gag gta aat gct tct cct tgg aat ctg gcc cat				1363
151	Ala Ser Ser Ala Glu Val Asn Ala Ser Pro Leu Trp Asn Leu Ala His				
152	330	335		340	

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153	gtg	aaa	atg	gag	cct	caa	gaa	agt	gaa	gaa	ggc	aat	gtc	tct	ggg	cat	1411
154	Val	Lys	Met	Glu	Pro	Gln	Glu	Ser	Glu	Glu	Gly	Asn	Val	Ser	Gly	His	
155				345					350						355		
156	ggt	gtg	ctg	ggc	agt	gat	gtc	ttc	gag	gag	cct	atg	tca	ggc	atg	agt	1459
157	Gly	Val	Leu	Gly	Ser	Asp	Val	Phe	Glu	Glu	Pro	Met	Ser	Gly	Met	Ser	
158				360				365						370			
159	gaa	gct	ggg	att	cct	cag	agc	cct	gat	gac	tca	gat	agc	agc	tat	ggt	1507
160	Glu	Ala	Gly	Ile	Pro	Gln	Ser	Pro	Asp	Asp	Ser	Asp	Ser	Ser	Tyr	Gly	
161		375				380						385					
162	tcc	cac	tcc	act	gac	agc	ctc	atg	ggg	tcc	tcc	cct	gtt	ttc	aac	cag	1555
163	Ser	His	Ser	Thr	Asp	Ser	Leu	Met	Gly	Ser	Ser	Pro	Val	Phe	Asn	Gln	
164	390				395						400				405		
165	cgc	tgc	aag	aag	agg	atg	agg	aaa	ata	taaaaggaaa	agagggagat						1602
166	Arg	Cys	Lys	Lys	Arg	Met	Arg	Lys	Ile								
167					410												
168	gttttgc	cca	gac	ctact	tag	acccaa	caga	aaagg	ttttt	gtatt	gaat	ctgttt	cctt				1662
169	aaaaatt	gtat	ttgact	cctg	ttctt	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa				1711
171	<210>	SEQ	ID	NO:	3												
172	<211>	LENGTH:	10														
173	<212>	TYPE:	PRT														
174	<213>	ORGANISM:	Homo sapiens														
176	<400>	SEQUENCE:	3														
177	Gly	Phe	Asp	Cys	Ala	Asn	Glu	Ser	Val	Leu							
178					5					10							
180	<210>	SEQ	ID	NO:	4												
181	<211>	LENGTH:	9														
182	<212>	TYPE:	PRT														
183	<213>	ORGANISM:	Homo sapiens														
185	<400>	SEQUENCE:	4														
186	Glu	Tyr	Cys	Leu	Lys	Phe	Thr	Lys	Leu								
187					5												
189	<210>	SEQ	ID	NO:	5												
190	<211>	LENGTH:	8														
191	<212>	TYPE:	PRT														
192	<213>	ORGANISM:	Homo sapiens														
194	<400>	SEQUENCE:	5														
195	Leu	Tyr	Gln	Ala	Val	Ala	Thr	Ile									
196					5												
198	<210>	SEQ	ID	NO:	6												
199	<211>	LENGTH:	9														
200	<212>	TYPE:	PRT														
201	<213>	ORGANISM:	Homo sapiens														
203	<400>	SEQUENCE:	6														
204	Ser	Phe	Asp	Leu	Leu	Pro	Arg	Glu	Phe								
205					5												
207	<210>	SEQ	ID	NO:	7												
208	<211>	LENGTH:	11														
209	<212>	TYPE:	PRT														
210	<213>	ORGANISM:	Homo sapiens														

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Input Set : A:\0020-4872P.ST25.txt  
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212 <400> SEQUENCE: 7  
213 Ser Phe Asp Leu Leu Pro Arg Glu Phe Arg Leu  
214 5 10  
216 <210> SEQ ID NO: 8  
217 <211> LENGTH: 9  
218 <212> TYPE: PRT  
219 <213> ORGANISM: Homo sapiens  
221 <400> SEQUENCE: 8  
222 Leu Tyr Gln Ala Val Ala Thr Ile Leu  
223 5  
225 <210> SEQ ID NO: 9  
226 <211> LENGTH: 10  
227 <212> TYPE: PRT  
228 <213> ORGANISM: Homo sapiens  
230 <400> SEQUENCE: 9  
231 Glu Tyr Cys Leu Lys Phe Thr Lys Leu Leu  
232 5 10  
234 <210> SEQ ID NO: 10  
235 <211> LENGTH: 10  
236 <212> TYPE: PRT  
237 <213> ORGANISM: Homo sapiens  
239 <400> SEQUENCE: 10  
240 Arg Phe Ala Val Asp Met Glu Gln Val Phe  
241 5 10  
243 <210> SEQ ID NO: 11  
244 <211> LENGTH: 10  
245 <212> TYPE: PRT  
246 <213> ORGANISM: Homo sapiens  
248 <400> SEQUENCE: 11  
249 Pro Phe Pro Asp Val Met Glu Gln Val Phe  
250 5 10  
252 <210> SEQ ID NO: 12  
253 <211> LENGTH: 11  
254 <212> TYPE: PRT  
255 <213> ORGANISM: Homo sapiens  
257 <400> SEQUENCE: 12  
258 Val Phe His Glu Val Gly Ile Gly Ser Val Leu  
259 5 10  
261 <210> SEQ ID NO: 13  
262 <211> LENGTH: 9  
263 <212> TYPE: PRT  
264 <213> ORGANISM: Homo sapiens  
266 <400> SEQUENCE: 13  
267 Asp Tyr His Ser Tyr Met Leu Gln Ile  
268 5  
270 <210> SEQ ID NO: 14  
271 <211> LENGTH: 10  
272 <212> TYPE: PRT  
273 <213> ORGANISM: Homo sapiens

Use of n and / or Xaa has been detected in the  
Sequence Listing. Review the Sequence Listing  
to ensure a corresponding explanation is present  
in the <220> to <223> fields of each sequence  
using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/857,308

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Input Set : A:\0020-4872P.ST25.txt  
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21

09857308 060304